Method for the *in vivo* modification of the synthesis activity of a metabolite by modification of a gene the activity of which is not the original activity

The present invention relates to a method for the *in vitro* and *in vivo* artificial evolution of proteins, said method making it possible to modify the activity of a protein X so as to obtain a mutant capable of acting on an analogue of the natural substrate. A mutant of N-deoxyribosyltransferase (DTP) was obtained, said mutation conferring acquisition of the N-dideoxyribosyltransferase activity.

Generally, the obtaining of enzymes having activities modified with respect to their natural activity is an important consideration since this would make it possible to have access to powerful tools in numerous industrial applications, in particular in biotechnology.

Various solutions for carrying out directed mutations in a DNA molecule have been described in the state of the art. These techniques consist of introducing *in vitro* a mutation, deletion or insertion into a determined site in a DNA molecule for example using PCR. These various techniques are described in Hall, et al. Protein Eng. 4: 601 (1991); Hemsley, et al. Nucleic Acids Research 17: 6545-6551 (1989); Ho, et al. Gene 77: 51-59 (1989); Hultman, et al. Nucleic Acids Research 18: 5107-5112 (1990); Jones, et al. Nature 344: 793-794 (1990); Jones, et al. Biotechniques 12: 528-533 (1992); Landt, et al. Gene 96: 125-128 (1990); Nassal, et al. Nucleic Acids Research 18: 3077-3078 (1990); Nelson, et al. Analytical Biochemistry 180: 147-151 (1989); Vallette, et al. Nucleic Acids Research 17: 723-733 (1989); Watkins, et al. Biotechniques 15: 700-704 (1993); Weiner, et al. Gene 126: 35-41 (1993). Yao, et al. PCR Methods and Applications 1: 205-207 (1992) and in Weiner and al, Gene 151: 1/9-123 (1994).

However, it is impossible to know in advance what is the effect of a given mutation on the activity of a protein with such techniques.

Other methods consist of introducing mutations into the genome at random by using mutagenic agents (2-aminopurine, hydroxylamine or ACRIDINE) and selecting the cells or organisms showing the sought phenotype. Nevertheless, these methods lead to the introduction of numerous

mutations, sometimes lethal, and are not suitable for causing a given protein to evolve for a precise purpose.

In order to respond to the needs and problems mentioned previously, the present invention proposes a method for modifying the activity of a protein combining *in vitro* and *in vivo* stages.

Within the framework of the invention it has been found that the introduction of mutations into the protein, followed by a confrontation with an analogue of the natural substrate within selective screening makes it possible to obtain a mutated protein having a strong activity on the new substrate. By repeating these operations, it is possible to obtain enzymes having an activity on substrates further and further removed from the initial natural substrate.

This method is particularly suitable for enzymes of the N-deoxyribosyltransferase (DTP) type.

Dideoxynucleosides such DDI and DDC and their derivatives are the most effective inhibitors known to date used in therapy against the HIV virus. These compounds are synthesized chemically, but can also be synthesized enzymatically. The N-deoxyribosyltransferase of *Lactobacillus leichmannii* (as well as that of *L. helveticus*), an enzyme which catalyzes the transfer of deoxyribose between two puric or pyrimidic bases is also capable of transferring 2',3'-dideoxyribose between these same bases (Carson and Wasson, 1988). Thus, several pyrazol (3,4-d) pyrimidine and triazolo (4,5-d) pyrimidine derivatives of 2',3'-dideoxycytidine and of the corresponding base have been synthesized (Fischer et al., 1990). The transfer reaction of 2',3'-dideoxyribose is however clearly less effective than that carried out with 2'-deoxyribose. For the purpose of having available an enzyme having a greater specific activity than the native enzyme for the transfer of 2', 3-dideoxyribose, we combined a stage of random mutagenesis of the *ntd* gene of *L. leichmannii* with a stage of selection of the mutants using genetic screening.

A functional screen making it possible to select the production of uracil has been established in *E. coli*, by deleting the *pyrC* gene which controls the conversion of carbamyl aspartate to dihydroorotate as well as the *codA* and *cdd* genes which respectively control the deamination of cytosine and (deoxy)cytidine in order to produce the strain PAK 9. The strain PAK 9 has a uracil (u) requirement which cannot be satisfied by supplying uridine (R-U),

deoxyuracil (dR-U) or dideoxyuracil (ddR-U). The use of dideoxyuracil (ddR-U) can however be selected in the strain PAK9 if a variant of N-deoxyribosyltransferase is capable of carrying out one of the following two reactions:

i) ddR-U $\longrightarrow$ U + ddR,

ii) ddR-U + C $\rightleftharpoons$ ddR-C + U.

A random mutagenesis of the *ntd* gene of *L. leichmannii* was carried out, the mutated products were then cloned in a plasmid and the mixture used for transforming the strain PAK9. The transforming clones were selected in glucose mineral medium to which dideoxyuracil (ddR-U) and cytosine (C) were added. Several transformants were obtained and are capable of carrying out the exchange

ddR-Pyr + Pur $\rightleftharpoons$ ddR-Pur + Pyr

as well as

dR-Pyr + Pur $\rightleftharpoons$ dR-Pur + Pyr.

The nucleotide sequences of the different variants of NTD are identical and differ from the wild-type gene only by one mutation. Their enzyme activities were evaluated from crude extracts or purified proteins. The specific activity of NTD* is 10 times less than that of NTD for the transfer of deoxyribose but is 7 times greater for the transfer of dideoxyribose.

The selected enzyme is used in the enzymatic synthesis of 2',3'-dideoxynucleotides with natural or modified bases (5-halogeno-pyrimidines), comprising or not comprising radioelements. The method can be extended to the selection of variants capable of transferring derivatives of 2'-deoxyribose or 2',3'-dideoxyribose between bases (such as 3'-amino-2',3'-dideoxyribose or 3'-azido-2,3'-dideoxyribose).

Moreover, in the method according to the invention, cells in which a metabolic pathway has been inactivated can be used. The selective target consists of complementing this deficiency by producing the product P for which the cells are auxotrophic from an analogue of the natural substrate of protein X.

Alternatively, a protein X can be evolved by complementation of a related protein Y, X and Y both belonging to the same class of the EC enzyme nomenclature or to neighbouring classes.

Description

Thus, generally, the present invention relates to a method for the artificial evolution *in vitro* and *in vivo* of proteins, said method making it possible to evolve a protein X *in vivo* by complementation either of a related protein, or by complementation of an inactivated metabolic pathway.

Such a method makes it possible to evolve a protein X so as to modify its characteristics and comprises the following stages:

a) obtaining mutants X* from the sequence coding for the protein X by random mutagenesis;

b) transformation of cells comprising a phenotype [P-] with vectors comprising the mutated nucleic acids obtained in stage a) coding for the proteins X*, P-signifying that said cells are auxotrophic for the substance P, P being the product of the action of X on its natural substrate S;

c) culture of said cells in a medium comprising a substrate S*, S* being an analogue of the natural substrate S of protein X;

d) selection of the cells [P-:: X*] which have survived stage c) in which the proteins X* are capable of carrying out the biosynthesis of the product P from the substrate S.

The mutant protein X* obtained is a protein having an activity close to the natural protein X, X* and X belonging to common or neighbouring enzyme classes having at least the first three figures of the 4-figure EC international nomenclature classes. In order to pass from one class to another, the above-mentioned method can be repeated with, at each passage, the addition of an additional modification to the substrate analogue designated by S*. By "substrate analogue" is meant the natural substrate S of natural protein X, comprising a modification or an alteration. By "modification" of this substrate is meant the addition or suppression of at least one atom, group or substituent, the modification of the spatial conformation of the substrate (isomer, enantiomer, diasteroisomer). This modification can be minimal or significant from the structural point of view. In this case, where it is sought to

substantially modify the activity of the protein (or enzyme), it is possible to repeat the method by further modifying the substrate S* at each new selection cycle. Little by little, the protein accumulates mutations which are responsible for the modification of its activity.

In this method, the cells used in stage b) are obtained by inactivation of at least one gene involved in the natural metabolic pathway leading to product P.

Thus, the obtained protein X* complements the deficiency of the natural metabolic pathway leading to product P in a medium provided with substrate S*.

By "complement" is meant the suppression of the auxotrophic phenotype resulting from the inactivation of the gene or the metabolic pathway.

Alternatively, the cells can be cells in which the gene coding for a protein related to X has been inactivated beforehand.

By "inactivation", is meant a deletion in whole or in part, an insertion, or a mutation rendering the gene inoperative. The inactivation can also consist of a modification leading to a Ts-type (temperature-sensitive) phenotype. In this case, the cells are cultured at temperatures which are not permissible for the selection phase (stages c) and d)).

Preferably, the related protein has at least the first three figures of the 4-figure EC international nomenclature.

Advantageously, the activity of protein X on substrate S is at least 2, 5, 10, 25, 50, 100 or 1000 times greater than its activity on substrate S*. In parallel, the activity of protein X* on substrate S* is at least 5, 10, 25, 50, 100 or 1000 times greater than its activity on substrate S.

Among the proteins referred to, there can be mentioned:

EC Number	**Name according to the international nomenclature**
-the ribosyltransferases, such as for example:	
2.4.2.5	Nucleoside ribosyltransferase.
2.4.2.6	Nucleoside deoxyribosyltransferase.
2.4.2.7	Adenine phosphoribosyltransferase
2.4.2.8	Hypoxanthine phosphoribosyltransferase.
2.4.2.9	Uracil phosphoribosyltransferase.

2.4.2.10	Orotate phosphoribosyltransferase.
2.4.2.11	Nicotinate phosphoribosyltransferase.
2.4.2.12	Nicotinamide phosphoribosyltransferase.
2.4.2.14	Amidophosphoribosyltransferase.
2.4.2.17	ATP phosphoribosyltransferase.
2.4.2.18	Anthranilate phosphoribosyltransferase.
2.4.2.20	Dioxotetrahydropyrimidine phosphoribosyltransferase.
2.4.2.21	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase.
2.4.2.22	Xanthine-guanine phosphoribosyltransferase.
2.4.2.29	Queuine tRNA-ribosyltransferase.
2.4.2.30	NAD(+) ADP-ribosyltransferase.
2.4.2.31	NAD(P)(+)--arginine ADP-ribosyltransferase.
2.4.2.36	NAD(+)--diphthamide ADP-ribosyltransferase.
2.4.2.37	NAD(+)--dinitrogen-reductase ADP-D-ribosyltransferase.

- the kinases, such as for example:

2.7.1.20	Adenosine kinase.
2.7.1.21	Thymidine kinase.
2.7.1.38	Phosphorylase kinase.
2.7.1.49	Hydroxymethylpyrimidine kinase.
2.7.1.74	Deoxycytidine kinase (DCK).
2.7.4.6	Nucleoside-diphosphate kinase.
2.7.4.7	Phosphomethylpyrimidine kinase.
2.7.4.8	Guanylate kinase.
2.7.4.9	Thymidylate kinase.
2.7.4.10	Nucleoside-triphosphate--adenylate kinase.
2.7.4.11	(Deoxy)adenylate kinase.
2.7.4.12	T2-induced deoxynucleotide kinase.
2.7.4.13	(Deoxy) nucleoside-phosphate kinase.

- the nucleotidyl transferases, such as for example

2.7.7.6	DNA-directed RNA polymerase.
2.7.7.7	DNA-directed DNA polymerase.

2.7.7.8 Polyribonucleotide nucleotidyitransferase.
2.7.7.19 Polynucleotide adenylyltransferase.
2.7.7.25 tRNA adenylyltransferase.
2.7.7.48 RNA-directed RNA polymerase.
2.7.7.49 RNA-directed DNA polymerase.
2.7.7.50 mRNA guanylyltransferase.

- the phosphorylases, such as for example

2.4.2.1 Purine-nucleoside phosphorylase.
2.4.2.2 Pyrimidine-nucleoside phosphorylase.
2.4.2.3 Uridine phosphorylase.
2.4.2.4 Thymidine phosphorylase.
2.4.2.7 Adenine phosphoribosyltransferase.
2.4.2.8 Hypoxanthine phosphoribosyltransferase.
2.4.2.9 Uracil phosphoribosyltransferase.
2.4.2.15 Guanosine phosphorylase.
2.4.2.23 Deoxyuridine phosphorylase.
2.4.2.28 5'-methylthioadenosine phosphorylase.

Preferably, protein X is selected from the ribosyltransferases belonging to the EC classes 2.4.2. -, in particular the N-deoxyribosyltransferases of EC class 2.4.2.6.

Of course, other enzymes, in particular the metabolism or catabolism enzymes, can be the subject of a modification using the method according to the invention. These enzymes and their respective EC number are indexed by the Committee of the International Union of Biochemistry and Molecular Biology (IUBMB) at the following address: http://expasy.proteome.org.au/enzyme/

The random mutagenesis of stage a) can be carried out either by variation of the manganese concentration during the PCR reaction, or by use of promutagenic nucleotide analogues or also by the use of primers comprising a random sequence. Different techniques are described in the documents US 6,323,030 (Methods for generating polynucleotides having desired characteristics by iterative selection and recombination), US 6,177,

263 (Recombination of polynucleotide sequences using random or defined primers), WO 01/66798 (Random truncation and amplification of nucleic acid), and EP1205547 (DNA mutagenesis by random fragmentation and reassembly).

The cells used within the framework of the invention are procaryotic or eucaryotic cells, preferably *E. coli.*

In a particular embodiment, the invention relates to a method as described above for evolving an N-deoxyribosyltransferase (DTP) so as to obtain an N-dideoxyribosyltransferase characterized in that it comprises the following stages:

a) obtaining DTP* mutants with the sequence coding for an N-deoxyribosyltransferase (DTP) by random mutagenesis;

b) transformation of cells comprising an [N-] phenotype with vectors comprising the mutated nucleic acids obtained in stage a) coding for the DTP* proteins, N- signifying that said cells are auxotrophic for at least one nucleoside, said nucleoside being the product of the action of DTP on its natural substrate dR-N;

c) culture of said cells in a medium comprising a substrate ddR-N;

d) selection of the [N-:: DTP*] cells which have survived stage c) in which the DTP* proteins are capable of carrying out the transfer of the dideoxyribose (ddR) from a dideoxyribonucleoside to another nucleoside leading to the production of the N nucleoside necessary for the survival of the cells.

By N nucleoside is meant a natural nucleoside, i.e. molecules constituted by a sugar bonded to a heterocyclic base by an N-glycosidic bond, the bases being pyrimidines (thymine, uracil, cytosine) or purines (adenine, guanine among the usual bases). By N-, is meant an [A-, T-, G-, C-, U- or I-] phenotype.

The NTD* enzyme obtained can be capable of recognizing and transferring a deoxyribose analogue such as dideoxyribose, but also acting on nucleoside analogues. Thus, the substrate analogue S* used can be a deoxyribonucleoside analogue comprising at least one chemical modification on the base and/or on the ribose.

More particularly, N-deoxyribosyltransferase (DTP) is the DTP of *Lactobacillus leichmannii* of SEQ ID No 1.

In this method, in stage b) *ΔpyrC, Δcod A, Δcdd E.coli* bacteria deficient in the metabolic pathway leading to uracil can be used. This bacterium is designated as being the PAK 9 strain deposited at the CNCM on 27th June 2002 under No. 1-2902.

In a second feature, the invention relates to the mutated protein X* capable of being obtained from the method described above, characterized in that it has a modified activity relative to the initial protein X.

The protein X* can be a mutated N-deoxyribosyltransferase capable of being obtained from the method according to the invention having an N-dideoxyribosyltransferase activity.

A subject of the present invention is also a mutated N-deoxyribosyltransferase capable of being obtained from the methods described above, characterized in that it has an N-dideoxyribosyltransferase activity and/or an activity on deoxy or dideoxyribonucleoside analogues comprising a modified base.

Advantageously, the invention relates to the abovementioned mutated N-deoxyribosyltransferase characterized in that it comprises the sequence SEQ ID No 2 comprising the mutation G9S and in that it has an N-dideoxyribosyltransferase activity.

The invention also relates to a nucleic acid comprising a sequence coding for the mutated N-deoxyribosyltransferase (NTD*) mentioned above, in particular the sequence SEQ ID No 3.

The invention also relates to an expression vector comprising said coding sequence. This sequence can be fused to an effective promoter in eucaryotic and/or procaryotic cells. The vector can be a plasmid capable of transforming and remaining in *E. coli*. The vector can remain in the bacterium in a stable or transitory manner.

The invention also relates to a host cell comprising a vector as described previously.

In a third feature, the invention relates to the use of an N-dideoxyribosyltransferase described above for the transfer of a dideoxyribose (ddR) from a dideoxyribonucleoside to another nucleoside. This enzyme

obtained from the method according to the invention is particularly useful for the preparation of nucleoside analogues having anti-tumorous properties, in particular ddI or ddC.

Thus, the invention also relates to a method for the preparation of compounds comprising a stage consisting of utilizing a mutated protein defined above.

This method is particularly advantageous for the preparation of nucleoside or nucleotide analogues useful for the treatment of cancer or infectious diseases, in particular dideoxyribonucleosides, in particular ddC or ddI.

The invention also relates to the PAK 9 strain of *E. coli* of genotype *ΔpyrC:: Gm, ΔcodA::Km, cdd::Tn10* deposited at the CNCM under accession number 1-2902.

Reference will be made to the legends of the figures hereafter in the remainder of the description.

Legends

- Figure 1: Biosynthesis routes
- Figure 1a) the "*de novo*" synthesis of DNA from simple precursors.
- Figure 1b) the backup or recycling route which is much less costly in terms of energy and involving reactions of sugar transfer from preformed bases (originating from the hydrolytic degradation of amino acids and nucleotides).
- Figure 2: Catalytic cycle of NTD
- Figure 3: Reaction ddU+I = ddI+U for psu-ntdA
- Figure 4: Reaction ddU+I = ddI+U for psu-ntd*C
- Figure 5: Reaction dU+I = dI+U for pSU-ntdA
- Figure 6: Reaction of dU +I = dI+U for pSU-ntd*C

EXAMPLE 1: Enzymatic synthesis of nucleosides

The synthesis of nucleosides in *E. coli* can be carried out according to two methods; [Agnete MUNCH-PETERSEN (1983). "Metabolism of nucleotides, nucleosides and nucleobases in microorganisms" published by Academic Press] (see Figures 1a and 1b).

Two classes of enzymes exist which catalyze the transfer of a 2-deoxyribosyl towards a nitrogenous base; see hereafter and [Jane R. HANRAHAN & David W. HUTCHINSON (1992). "The enzymatic synthesis of antiviral agents". Journal of Biotechnology; vol. 23; 193-210. The latter are sometimes used for the synthesis of nucleoside analogues].

1.1 The nucleoside phosphorylases

See the article by [Thomas A. KRENITSKY, George W. KOASALKA & Joel TUTTLE (1981). "Purine nucleoside synthesis, an efficient method employing nucleoside phosphorylase". Biochemistry; vol. 20; 3165-3621].

The majority of the microorganisms (such as *E. coli*) use this synthesis route which commences with the "reversible" phosphorylation of a ribonucleoside to ribose-1-phosphate (or 2-deoxyribonucleoside to 2-deoxyribose-1-phosphate) from inorganic phosphate with release of the donor base (1) followed by the addition of the acceptor base (2).

(1): (d)R-Base1 + H_2PO_4 $\rightleftharpoons$ (d)R-1-phosphate + $Base_1$

(2): (d)R-1-phosphate+ $Base_2$ $\rightleftharpoons$ (d)R-Base2 + H_2PO_4.

(3) = (1) + (2): (d)R-$Base_1$ + $Base_2$ $\rightleftharpoons$ $Base_1$ + (d)R-$Base_2$

(d)R =(2-deoxy) ribose

[E] = PNPase (purine phosphorylase) or Deo D for Base = purine
Urd Pase (uridine phosphorylase) or UDP for Base = U (and T in marginal fashion)
dThd Pase (thymidine phosphorylase) or Deo A for Base = T (and U in marginal fashion)

These enzymes catalyze the same reaction with different substrates.

However, two classes of enzymes are distinguished [A.R. MUSHEGIAN & E.V. KOONIN (1994). "Unexpected sequence similarity between nucleosidases and phosphoribosyltransferases of different specificity". Protein Science; vol. 3; 1081-1088]:

- on the one hand family I to which Deo D and UDP are attached (in *E. coli* the amino acid sequences which constitute them are very similar);
- on the other hand family II comprising thymidine phosphorylases. Enzymes having the same function and being able to fix the same substrate (such as UDP and Deo A) do not therefore necessarily have related amino acid sequences.

1.2 The N-deoxyribosyltransferases (NTD)

The N-deoxyribosyltransferases catalyze the cleavage of the glycosidic bonds of the 2-deoxynucleotides. They are present in certain microorganisms which have little or no purine and pyrimidine phosphorylase (lactobacilla for example) [6-8]. They participate in the recycling of nucleotides.

Catalyzed reactions according to the type of enzymes

Two types of enzyme have been characterized, [José HOLGUIN & Robert CARDINAUD (1975). "Trans-N-Deoxyribosylase: substrate specific studies". European Journal of Biochemistry; vol. 54; 515-520].

Purine deoxyribosyltransferase or NTD I:

This exclusively catalyzes the reversible transfer of a sugar with a puric base (donor base) to another purine (acceptor base).

(1): $(d)R\text{-}pur_1 + pur_2 \rightleftharpoons pur_1 + (d)R\text{-}pur_2$

Pyrimidine/Purine deoxyribosyltransferase or NTD II:

This mostly catalyzes the transfer between purine and pyrimidine according to the following reversible equations:

(2): (d)R-pyr_1 +pyr_2 $\rightleftharpoons$ pyr_1 +(d)R-pyr_2

(3): (d)R-pyr_1 +pur_2 $\rightleftharpoons$ pyr_1 +(d)R-pur_2

Reaction mechanism (Figure 2)

NTD II of *Lactobacillus delbruckii* would react according to a "ping-pong-bi-bi" mechanism which would involve two substrates and two products [José HOLGUIN & Robert CARDINAUD (1975). "Trans-N-Deoxyribosylase: Purification by affinity chromatography and characterization". European Journal of Biochemistry; vol. 54; 505-514; C. DANZIN & Robert CARDINAUD (1974). "Deoxyribosyl transfer catalysis with trans-N-deoxyribosylase. Kinetic studies of purine to purine trans-N-deoxyribosylase. European Journal of Biochemistry; vol. 48; 255-252; C. DANZIN & Robert CARDINAUD (1976). "Deoxyribosyl transfer catalysis with trans-N-deoxyribosylase. Kinetic studies of purine (pyrimidine) to purine (pyrimidine) trans-N-deoxyribosylase. European Journal of Biochemistry; vol. 62; 356-372].

It is assumed that the sugar of the donor nucleoside ($dBase_1$) binds to the enzyme in a covalent manner. An intramolecular reaction within this binary complex allows the cleavage of the β-glycosidic bond and the formation of a ternary complex E-deoxyribosyl-$Base_1$ followed by the release of the first product ($Base_1$). The acceptor base ($Base_2$) then binds to the binary intermediate and after intramolecular reaction on the active site of the enzyme, the second product ($dBase_2$) is released. The enzyme can then lead to another catalysis.

Physico-chemical properties

The two enzymes have a similar molecular weight (evaluated at approximately 100 kDa) but they differ in their heat stability (activity observed up to 45°C for NTD I and 55°C for NTD II) and their optimum pH (6.4 for NTD I and 6.0 for NTD II).

The *ntd* gene of *Lactobacillus delbruckii* coding for NTD II with a length of 471 bp codes for the synthesis of a protein with 157 amino acids and a total molecular weight of 110 kDa [William J. COOK, Steven A. SHORT & Steven E.

EALICK (1990). "Crystallization & preliminary X-ray investigation of recombinant *Lactobacillus leichmanii* nucleoside 2-deoxyribosyltransferase". The Journal of Biological Chemistry; vol. 265; No. 5; 2682-2683]. The crystalline structure of the NTD II enzyme of *L. delbruckii* was determined with a resolution of 2.5 Å. This is a hexamer (trimer of dimers) constituted by six identical sub-units of 18 kDa. Each sub-unit has at its centre a parallel β sheet comprising five strands of various lengths and surrounded by four α helices arranged asymmetrically. Each one comprises an active site, but the six catalytic centres, in pairs separated by approximately 20 Å, require the participation of the side chains of the neighbouring sub-units [Shelly R. ARMSTRONG, William J. COOK, Steven A. SHORT & Steven E. EALICK (1996). "Crystal structures of nucleoside 2- deoxyribosyltransferase in native & ligand-bound forms reveal architecture of the active site". Structure; vol.4; No.1; 97-107]. The latter are involved in the positioning of the catalytic amino acid (glutamate 98) [David J. T. PORTER, Barbara M. MERRIL & Steven A. SHORT (1995). "Identification of the active site nucleophilic nucleoside 2-deoxyribosyltransferase as glutamic acid 98". The Journal of Biological chemistry; vol. 270; No. 26; 15551-15556].

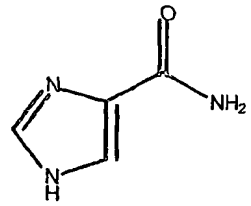
Enzymatic synthesis of nucleoside analogues

The transfer reactions, which are highly stereospecific, in the presence of an NTD I or NTD II transferase, exclusively produce the β anomer of the nucleoside (which avoids the stage of separation of the α and β isomers).

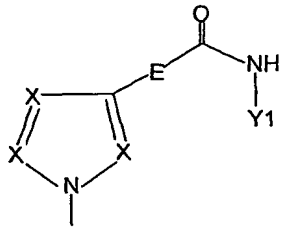
The enzyme has a great specificity vis-à-vis 2'-deoxyribonucleotides but tolerates a large number of modified analogues on the sugar or on the base. Thymidine and cytosine seem to be the most effective sugar donors. On the other hand the transfer can be carried out on a large panel of acceptor bases. The purines substituted in position 6 should for example be mentioned [D. BETBEDER, D.W. HUTCHINSON & A.O. RICHARDS (1989). "The stereoselective enzymatic synthesis of 9-β-D-2',3'dideoxynucleosides of N(6)-substitued purines". Antiviral Chem. Chemother; vol. 17; 4217-4222] and dYTP.

dYTP:

The imidazole-4-carboxamide called Y has been proposed as simplified purine. This analogue has the formula:



It has been reported that the nucleotide dYTP could be substituted for dATP or dGTP during the copying of the DNA which introduces mutations. There can also be mentioned the compounds described in WO 01/96354 (Institut Pasteur) of general formula:



The NTD enzymes are shown to be capable of marginally catalyzing the exchange reaction between a 2',3'-dideoxyribose and an acceptor base:

$$\text{dd-1'-Base}_1 + \text{Base}_2 \rightleftharpoons \text{Base}_1 + \text{dd-1'-Base}_2$$

dd = 2',3'-dideoxyribose

Nevertheless the speed of this transfer remains very low compared with that characterizing the exchange of deoxyriboses.

The 2',3'-dideoxyribonucleotides are evidently useful as chain terminators in the sequencing procedures. Moreover, 2',3'-dideoxyadenosine (ddA) and 2',3'-dideoxyinosine (ddI) are used for therapeutic purposes in particular in the case of the AIDS virus: these analogues effectively inhibit the replication of HIV (human immunodeficiency virus) [H. MITSUYA & S. BRODER (1987). "Strategies for antiviral therapy in AIDS". Nature; vol. 325; 773-778].

To this end, the invention provides a novel method for obtaining mutants of the NTD II enzyme in order to select mutant enzymes which have a

stronger specificity vis-à-vis the 2',3'-dideoxyribonucleosides than the native enzyme.

EXAMPLE 2: Use of the method according to the invention for obtaining NTD*

MATERIALS AND METHODS

E. coli strains are cultured in Luria-Bertani (LB) medium or in MS minimum medium (Richaud et al. 1993). The antibiotics kanamycin, Km, chloramphenicol Cm, are used at a final concentration of 25 µg/ml; tetracycline, Tc and gentamycin, Gm, 10 µg/ml. The nucleosides and bases are used in the culture media at a final concentration of 0.3 mM. The molecular biology techniques were carried out according to Sambrook et al. (1989).

The amplification products are purified using QIAquick PCR purification (QIAgen).

The DNA fragments purified on agarose gel are extracted using the Jetsorb Kit (Genomed) or the QIAquick gel extraction kit (QIAgen). The plasmid DNA is purified using the QIAprep Spin Miniprep kit (QIAgen)

1- Construction of the strain PAK9 (MG1655ΔpyrC:: Gm, ΔcodA::Km, cdd:: Tn10)

*** ΔcodA::Km:**

The oligonucleotides codBL (5'-NNNCCCGGGCTTCTTGCTCGCTTCTCGTTTGG-3') (SEQ ID No 4) and cynTR (5'-NNGGATCCGTTTGACCGTAGCGGGCGAAC-3') (SEQ ID No 5) were used in order to amplify, starting from the DNA of the *E.coli* strain MG1655, a fragment of 3.3kb containing the *pyrC* gene.

The PCR reactions are carried out in a final volume of 100 µL comprising 100 pmol of each oligonucleotide, 700 ng of DNA of the strain MG1655, the dNTPs at a final concentration of 200µM, 10 µL of 10 times concentrated *Taq* polymerase reaction buffer (Roche) and 5 U of *Taq* polymerase (Roche). The amplification parameters are:

1 5-second cycle at 95°C, 25 cycles each comprising the following three stages: 30 seconds at 95°C, 30 seconds at 60°C, 2 minutes at 72°C, then a 10-minute cycle at 72°C. The amplification product was then digested by the restriction enzymes *Xma*I and *Bam*HI, purified on gel and ligated to the pMTL22 plasmid (Chambers et al. 1988) digested by the same enzymes and purified on gel as above. The ligature mixture was used to transform the strain β 2033. The plasmid DNA of several transformants was prepared and used as DNA matrix in order to delete the *codA* gene using the oligonucleotides codBR (5'-NGAATTCTTATTCGACACTGTTAGCCTCC-3') (SEQ ID No 6) and cynTL (5'-NGAATTCACGACTGGGTTACAGCGAGC-3') (SEQ ID No 7) under the same conditions and with the same parameters as above. The amplification product was then digested by the restriction enzyme *Eco*RI, purified on agarose gel and ligated to the *Eco*RI fragment of 1.2 kb of pUC4K (Pharmacia) conferring resistance to kanamycin. The ligature mixture was used in order to transform the strain β 2033. The plasmid DNA of several transformants resistant to kanamycin was prepared then used as DNA matrix for an amplification reaction with the oligonucleotides codBL and cynTR. The amplification product was then purified on agarose gel, digested by the restriction enzyme *Dpn*I for 12 hours at 37°C then extracted with phenol and precipitated from ethanol. The DNA taken up in solution in water was used in order to transform the strain MG1655 hosting the pKOBEG plasmid by electroporation (donated by J-M Ghigo, Unité des membranes bacteriennes). The transformant clones obtained on LB medium in the presence of kanamycin were then tested for sensitivity to 5-fluorouracil and resistance to 5-fluorocytosine. The deletion of the gene *codA* was also verified by amplification with the oligonucleotides codBL and cynTR.

*** Δ*pyrC*::Gm:**

The oligonucleotides
ycEL (5'-NNNCCCGGGGCCGACCTGCTGGCCCACTCTGACGG-3')
(SEQ ID No 8) and
dinR (5'-NNGGATCCCCCGGCGGCAGCGCCTACGGAACCGCTGCC-3')
(SEQ ID No 9)

were used in order to amplify, starting from the DNA of the *E. coli* strain MG1655, a fragment of 3.1 kb containing the *pyrC* gene according to the protocol described for *codA*. The amplification product was then inserted into the pCR2.1-TOPO plasmid (Invitrogen, USA) and the mixture used to transform the strain TOP10F' (Invitrogen, USA). The plasmid DNA of the transformant clones was then prepared and used as matrix in an amplification reaction with the oligonucleotides

yceR (5'-NGAATTCTTAATCAGTAAATGGAATGACAATTTCGCC-3')
(SEQ ID No 10) and

dinL (5'-NGAATTCAAATCGTAGCTTCCTGTTGTCATTAGG-3')
(SEQ ID No 11).

The amplification parameters 1 5-second cycle at 95°C, 25 cycles each comprising the following three stages: 30 seconds at 95°C, 30 seconds at 65°C, 3 minutes at 72°C, then a 10-minute cycle at 72°C. The amplification product was then digested by the restriction enzyme *Eco*RI purified on gel and ligated to an *Eco*RI fragment of 1.1 kb conferring resistance to gentamycin. The ligature mixture was used to transform the strain β 2033.The plasmid DNA of the transformant clones resistant to gentamycin was then prepared and used in an amplification reaction with the oligonucleotides yceL and dinR. The amplification product was then purified on agarose gel then digested by the restriction enzyme *Dpn*I for 12 hours at 37°C and precipitated from ethanol after phenol extraction. The DNA was resolubilized in water then used to electroporate the strain MG1655 hosting the pKOBEG plasmid. The transformant clones were obtained on LB medium in the presence of gentamycin and uracil. The clones auxotrophic for uracil were also deleted from the *pyrC* gene.

*** Δ*pyrC*::Gm, Δ*codA*::Km, *cdd*::*Tn*10.**

The *codA*::Km mutation carried by the strain PAK1 was transduced into the strain PAK2 (MG1655 Δ*pyrC*::Gm) using phage P1. The transductants were selected on LB medium supplemented with kanamycin, gentamycin and uracil. In the same manner the *cdd*::*Tn*10 was introduced into the strain PAK15 (MG1655 Δ*pyrC*::Gm, Δ*codA*::Km) by transduction using a phage P1 stock prepared from the strain β7234 Δ*deo*, *argE*::*am* *cdd*::*Tn*10). The

transductants were selected on the medium described above supplemented with tetracycline which made it possible to isolate the strain PAK9 (MG1655 Δ*pyrC*::Gm, Δ*codA*::Km, *cdd*::*Tn*10). The strain PAK9 is auxotrophic for uracil (U), uridine (rU), and 2'-deoxycytidine (dC) and is incapable of growing on minimum mineral medium supplemented with glucose and cytosine (C), cytidine (rC) or 2'-deoxycytidine (dC).

2 - Mutagenesis

2.1 Variation in the manganese concentration during the PCR reaction

The primers FP23 (5'-CGCCAGGGTTTTCCCAGTCACG) (SEQ ID No 12) and RP23 (5'-AGCGGATAACAATTTCACACAGG) (SEQ ID No 13) were used in order to amplify the cloned *ntd* gene in the pSU19 plasmid according to standard amplification conditions except for the final concentration of dNTPs: 20 µM and the Mn^{2+} ion concentration which varies from 0 to 0.5 mM final according to the experiments. The amplification parameters 1 5-minute cycle at 95°C, 40 cycles each comprising the following three stages: 30 seconds at 95°C, 30 seconds at 53°C, 3 minutes at 72°C, then a 10-minute cycle at 72°C.

2.2 Mutagenesis by incorporation of a dYTP purine analogue

Different amplification reactions were carried out using the oligonucleotides RP23 and FP23 as primers, the pSU19 plasmid containing the *ntd* gene as DNA matrix. In order to substitute the dATP, the following concentrations were used: dYTP (1mM), dATP, dCTP and dTTP (200 µM) dGTP varying from 1 to 5 µM. In order to substitute the dGTP, the following concentrations were used: dYTP (1mM), dATP, dCTP and dTTP (200 µM) dGTP varying from 1 to 5 µM. The amplification parameters are the same as those which are described above except for the third stage where the extension time is 10 minutes. A second amplification reaction is then carried out under the standard conditions using 10 µL of the first amplification.

3- Cloning and selection

The purified amplification products are digested over 2 hours at 37°C by the restriction enzymes *BamH*I and *Hind*III. After migration at 150 V over 45

minutes, they are purified by 1% agarose gel extraction using the QIAquick gel extraction kit (QIAgen).

The pSU19 plasmid is digested by the same enzymes and purified according to the same procedure.

The ligatures carried out in a volume of 20 µL include 15 ng of the amplification products, 50 ng of pSU19 digested by *BamH*I-*Hind*III, 2 µL of 10x concentrated T4 DNA ligase reaction buffer and 6 U of T4 DNA ligase. The reaction is carried out at 16°C over 18 hours.

The ligature products are then dialyzed on Millipore filter (0.05 µm; 13 mm) for 30 minutes then used in order to transform the strain PAK9, prepared according to the protocol described by Dower et al. (1987), by electroporation.

1 to 5 µL of ligated DNA mixed with 50 µL of the strain PAK9 in a 2-mm cuvette are subjected to a 2.5 kV charge. After incubation for an hour at 37°C in 1 ml of LB medium supplemented with uracil (0.3 mM), two successive washings with 1x 1 ml MS medium are carried out.

450 µL of suspension are plated on glucose mineral agar medium supplemented with Cm, ddU and C. The dishes are incubated at 37°C over 4 days. The selected colonies are then isolated on the same medium.

The plasmid DNA of the isolated colonies is prepared from culture in LB medium supplemented with Cm and U. Sequencing was carried out by MWG-BIOTECH.

4-Measurement of the enzymatic activity of the crude extracts of the different mutants

4.1 Preparation of the crude extracts

The precultures are obtained after inoculation of an isolated colony in 5 mL of LB medium containing Cm and U for the strain PAK9 followed by incubation overnight under stirring at 37°C.

The next day, 15 mL of LB medium, Cm and U are inoculated at an OD_{600} = 0.01. The cultures are then incubated at 37°C until an OD comprised between 0.8 and 1 is reached.

The cells are then centrifuged at 4,000 rpm for 30 minutes at 4°C, the pellet is resuspended in 10 ml of 50 mM phosphate buffer (Na_2HPO_4 + NaH_2PO_4) (pH = 7.5). After centrifugation, the pellet is resuspended in 1 ml of

the same buffer. The cells, preserved in ice, then undergo three 30-second cycles of sonication and 30-second cycles of rest. After centrifugation at 12,000 rpm for 2 x 15 minutes at 4°C; the supernatants are recovered and stored at -20°C.

4.2 Enzymatic reaction

50 µL of enzyme extract are added to 200 µL of 100 mM citrate buffer, pH 6.44, in the presence of ddU or dU at 3 mM final and of C at 1 mM final for the strain PAK9, the whole is incubated at 37°C. The progress of the reaction is monitored by TLC (Silica; eluent: MeOH-CH_2Cl_2 (20/80)). The products are developed under UV, and the sugars developed by Zücker reagent. The disappearance of the substrates and the formation of the products are also quantified by HPLC analysis. The different products are separated by analytical HPLC with a reversed-phase column (100-5C18) using a flow rate of 1 ml/min and a CH_3CN 5-25% linear gradient in a 10 mM triethylammonium acetate buffer at pH 7.5 for 20 minutes.

5- Overproduction and purification of the native *N*-deoxyribosyltransferase and LL7 mutant.

The oligonucleotides
5'-GATATACATATGCCAAAAAAGACGATCTAC (SEQ ID No 14) and
5'-NNGGATCCTTAGTATACGGCACCTTCGTAGAAGTCG (SEQ ID No 15)
were used as primer in an amplification reaction under standard conditions using the cloned *ntd* gene in pSU19 or mutant 7 previously selected as DNA matrix. Each amplification product was digested by the restriction enzymes *Nde*I and *BamH*I for 2 hours at 37°C, purified on agarose gel and inserted into the pET24a plasmid (NOVAGEN) digested by the same enzymes, then the ligature mixture used to transform the strain β 2033. The plasmid DNA of the colonies was prepared and digested by the enzymes *Nde*I and *Bam*HI. Those the sequence of which was correct were used in order to transform the strain BL21 (DE3)/pLYS (NOVAGEN). The overproduction of the two enzymes was obtained from cultures of 500 ml of LB medium supplemented with Km and Cm. These cultures were induced at an OD_{600} = 1 by the addition of IPTG (0.4 mM), the incubation being continued for 2 hours at 37°C.

The cells are then centrifuged for 15 minutes at 4000 rpm at 4°C, washed in 50 ml of phosphate buffer then the pellet obtained after centrifugation is stored overnight: at -20°C. The bacterial pellet resuspended in 20 ml of phosphate buffer is then lyzed by passing through a French press at 14000 psi. The lysate is centrifuged for 90 minutes at 50,000 rpm. The supernatant containing the soluble proteins is then precipitated with ammonium sulphate (55% saturation). The precipitate obtained after centrifugation at 13,900 rpm (20,000 g) for 30 minutes at 4°C is resuspended in 5 ml of 100 mM phosphate buffer, pH 7.5, then dialyzed overnight at 4°C against the same buffer at pH 6.0. The enzyme extract is then heated at 60°C for 5 minutes then immediately replaced in ice. The denatured proteins are eliminated by centrifugation at 20,000 rpm for 30 minutes at 4°C. The purity of each enzyme is then analyzed by SDS-PAGE gel and the concentration determined by Bradford assay using a BSA range as standard. The measurement of the enzyme activities is carried out as described in paragraph 4.2.

RESULTS

Activity tests of enzymatic extracts

The activity present in the prepared enzymatic extract is assayed following the appearance of the product on TLC. Two types of reaction are tested depend on whether the transferred sugar is a deoxyribose or a dideoxyribose.

After incubation for 3 hours at 37°C, only the mutant extracts catalyze the transfer reaction

ddU + C → ddC + U.

Like the wild-type strain, they are also capable of transferring deoxyribose but at an apparently slower speed.

On the other hand the reactions

ddU + I → ddI + U

as well as

ddT + C → ddC + T

have also produced positive results with these four extracts. These results show that with a dideoxypyrimidine as donor, the acceptor base can be a purine or a pyrimidine.

Moreover, the extracts originating from the various mutants seem to behave in the same manner. We pursued the kinetic study more particularly on the mutant pSU-*ntd**C by comparing its activity to that of the wild-type strain pSU-*ntd*A using HPLC analyses.

Kinetic monitoring of the reactions at pH = 7.5

We chose to consider reactions (1) and (2) and to take dU or ddU as donor and hypoxanthine I as acceptor.

(1) *dU + I = dI + U*

(2) *ddU + 1 = ddi + U*

The donor nucleosides are introduced in excess relative to the acceptor base (in a ratio of 3:1) in order to shift the equilibrium of the reactions in the direction of the sugar transfer.

HPLC analysis allows precise monitoring of the progress of the reaction as a function of time. The reaction products are characterized by a retention time t (given for a gradient of 0 to 15 of acetonitrile in a buffer over 20 minutes). Detection is carried out at 254 nm.

	U	I	dU	dI	ddU	ddI
t (min)	3.8	6.7	7.8	9.3	10.4	11.9

Reaction (1): transfer of deoxyribose

As shown in Figure 3, the N-deoxyribosyltransferase NTD II of pSU-*ntd* A rapidly catalyzes this exchange: the formation of U and dI is virtually immediate. After one hour at 37°C, more than 70% of hypoxanthine I (limiting reagent) has reacted and the formation of dI is noted. After four hours; 88% of I introduced initially with a view to producing dI and U has been consumed.

The mutant strain is also capable of carrying out the exchange of deoxyribose but with much slower kinetics than the wild-type strain. An hour at 37°C is necessary before the appearance of the products: approximately 30% of I have then been transformed (Figure 4). Even if the reaction proves to be slower, equilibrium is reached after twelve hours in both cases.

Reaction (2): transfer of dideoxyribose

No conversion of ddU to ddt is obtained with the extracts expressing the wild-type *ntd* gene, even after 24 hours at 37°C (Figure 5).

On the other hand, with the extracts expressing the mutated gene, after one hour N-deoxyribosyltransferase catalyzes the formation of ddI and U with 25 % of hypoxanthine having reacted (Figure 6). Figure 6 shows the relative proportions of the reagents and of the products for the two strains after three hours at 37°C. In the case of the extract containing the mutant enzyme after the consumption of more than 50% of I over four hours the reaction diminishes. No shifting of the equilibrium reached is detected after 24 hours. The reaction is shown to be virtually total (more than 90% of I has reacted in order to synthesize ddI and U). On the other hand with the control strain only 5 % of synthesizable ddI is produced.

The NTD* enzyme produced by the pSU-*ntd**C plasmid proves to be an excellent catalyst of the exchange reaction vis-à-vis 2',3'-dideoxyribose. Two major features have been modified: the speed has clearly increased and the state of equilibrium is broadly shifted in favour of the transfer of 2',3'-dideoxyribose. Thus the reaction has become both rapid and quantitative.

CONCLUSION

Different random mutagenesis protocols were tested with a view to modifying the specificity of N-deoxyribosyltransferase vis-à-vis the dideoxyriboses. The first is based on alteration of the fidelity of the *Taq* polymerase in the presence of manganese, which under the tested conditions (0.25 mM) generates a limited number of mutations per clone. The second protocol is based on the use of a nucleoside analogue, dYTP, instead of dGTP which is described in order to generate a low level of mutations. It would therefore seem that the conversion of an N-deoxyribosyltransferase activity to an N-dideoxyribosyltransferase activity requires only one or two mutations.

The number of mutants retained after the stage of selection on a dish remains very low compared with the total number of mutants generated. This observation underlines the power of a selection based on nutritional requirements.

On the other hand the mutated N-deoxyribosyltransferases NTD* expressed in the strain Δ*pyrC* Δ*codA* Δ*cdd* can catalyze various exchange reactions such as:

ddU + C = ddC + U;
ddT + C = ddC + T and
ddU + I= ddI +U.

A kinetic study of this last reaction shows that the speed of transfer of dideoxyribose by the mutated enzyme has been increased by at least a factor of 10 compared with that of the wild-type enzyme.

Moreover, the reaction catalyzed by the N-deoxyribosyltransferase NTD* can be considered as rapid and total with more than 90% of the limiting reagent consumed.

The mutated enzyme is also capable of catalyzing the exchange of deoxyribose but at a reaction speed reduced by half compared with that observed for the native enzyme. Moreover, it is possible to imagine the reiteration of an evolution directed to the mutated genes. Thus, an enzymatic synthesis of antiviral agents catalyzed by these mutated enzymes could be envisaged. This perspective would simplify the preparation of the dideoxynucleotides, obtained in general by reduction of the corresponding deoxynucleotides.

The method of random mutagenesis associated with a selection phase is applicable to numerous genes coding for example for the synthesis of biologically useful products. It opens up a prodigious variability of genes mutated from a single gene and can thus make it possible to improve an activity already existing in certain enzymes or even to generate a new activity.

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